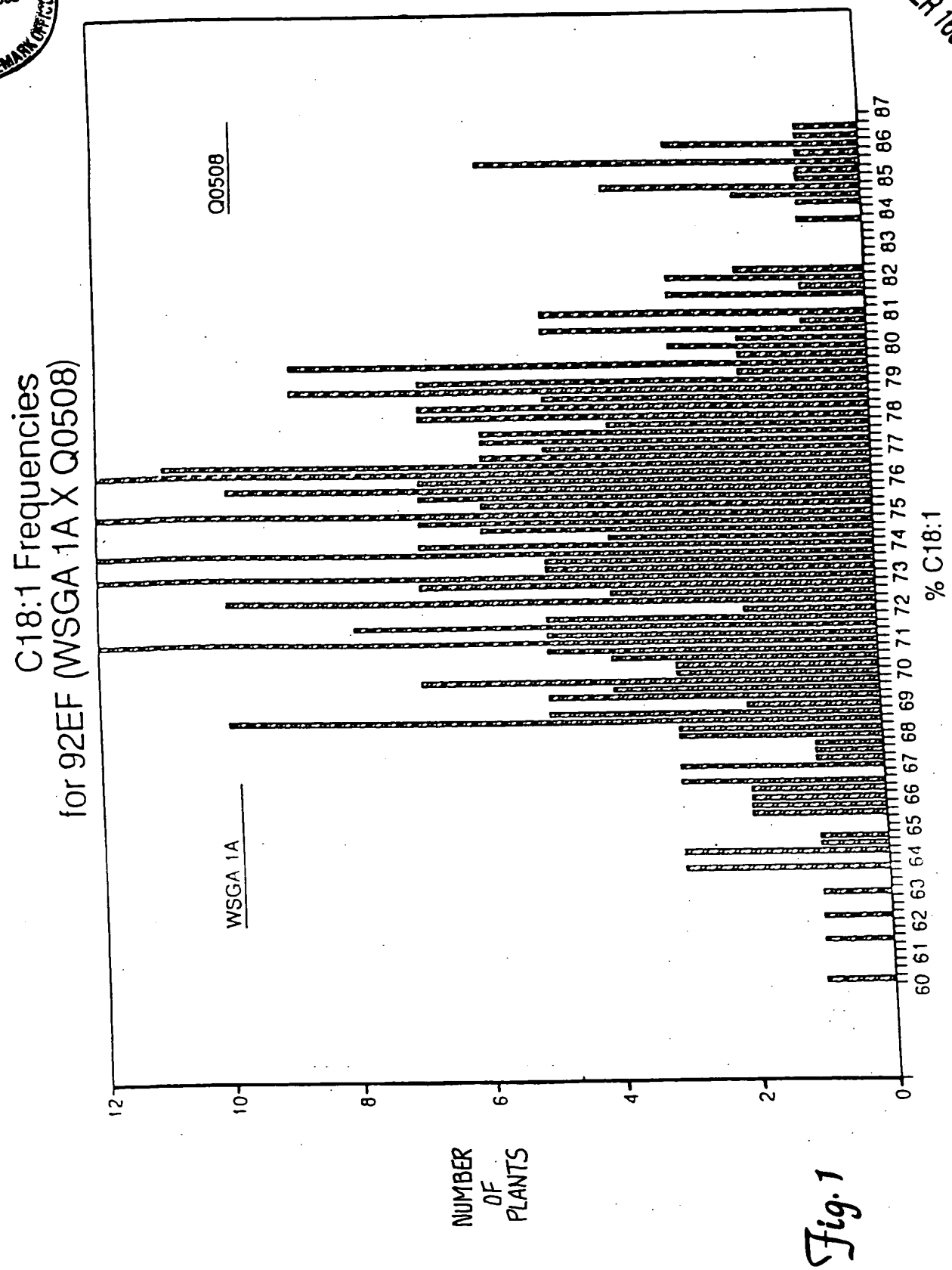

Fig. 1

Start	Sequence (positions 1–40)	Name
1	ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCA	Fad2-D wt
1	ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCA	Fad2-D (GA316) IMC 129
1	ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCA	Fad2-F wt
1	ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCA	Fad2-F (TA515) Q508
1	ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCA	Fad2-F (GA908) Q4275

Start	Sequence (positions 41–80)	Name
41	AAAAGTCTGAAACCGACAACATCAAGCGCGTACCCTGCGA	Fad2-D wt
41	AAAAGTCTGAAACCGACAACATCAAGCGCGTACCCTGCGA	Fad2-D (GA316) IMC 129
41	AGAAGTCTGAAACCGACACCATCAAGCGCGTACCCTGCGA	Fad2-F wt
41	AGAAGTCTGAAACCGACACCATCAAGCGCGTACCCTGCGA	Fad2-F (TA515) Q508
41	AGAAGTCTGAAACCGACACCATCAAGCGCGTACCCTGCGA	Fad2-F (GA908) Q4275

Start	Sequence (positions 81–120)	Name
81	GACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATC	Fad2-D wt
81	GACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATC	Fad2-D (GA316) IMC 129
81	GACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATC	Fad2-F wt
81	GACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATC	Fad2-F (TA515) Q508
81	GACACCGCCCTTCACTGTCGGAGAACTCAAGAAAGCAATC	Fad2-F (GA908) Q4275

Start	Sequence (positions 121–160)	Name
121	CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCT	Fad2-D wt
121	CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCT	Fad2-D (GA316) IMC 129
121	CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCT	Fad2-F wt
121	CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCT	Fad2-F (TA515) Q508
121	CCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCT	Fad2-F (GA908) Q4275

Fig. 2A

Start	Sequence (161–200)	Line
161	CCTACCTCATCTGGGACATCATCATAGCCTCCTGCTTCTA	Fad2-D wt
161	CCTACCTCATCTGGGACATCATCATAGCCTCCTGCTTCTA	Fad2-D (GA316) IMC 129
161	CCTACCTCATCTGGGACATCATCATAGCCTCCTGCTTCTA	Fad2-F wt
161	CCTACCTCATCTGGGACATCATCATAGCCTCCTGCTTCTA	Fad2-F (TA515) Q508
161	CCTACCTCATCTGGGACATCATCATAGCCTCCTGCTTCTA	Fad2-F (GA908) Q4275

Start	Sequence (201–240)	Line
201	CTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCT	Fad2-D wt
201	CTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCT	Fad2-D (GA316) IMC 129
201	CTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCT	Fad2-F wt
201	CTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCT	Fad2-F (TA515) Q508
201	CTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCT	Fad2-F (GA908) Q4275

Start	Sequence (241–280)	Line
241	CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGG	Fad2-D wt
241	CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGG	Fad2-D (GA316) IMC 129
241	CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAAG	Fad2-F wt
241	CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAAG	Fad2-F (TA515) Q508
241	CTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAAG	Fad2-F (GA908) Q4275

Start	Sequence (281–320)	Line
281	GCTGCGTCCTAACCGGCGTCTGGGTCATAGCCCACGAGTG	Fad2-D wt
281	GCTGCGTCCTAACCGGCGTCTGGGTCATAGCCCACAAGTG	Fad2-D (GA316) IMC 129
281	GGTGCGTCCTAACCGGCGTCTGGGTCATAGCCCACGAGTG	Fad2-F wt
281	GGTGCGTCCTAACCGGCGTCTGGGTCATAGCCCACGAGTG	Fad2-F (TA515) Q508
281	GGTGCGTCCTAACCGGCGTCTGGGTCATAGCCCACGAGTG	Fad2-F (GA908) Q4275

Fig. 2B

```
                330        340        350        360
321 CGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGACGAC Fad2-D wt
321 CGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGACGAC Fad2-D (GA316) IMC 129
321 CGGCCACCACGCCTTCAGCGACTACCAGTGGCTTGACGAC Fad2-F wt
321 CGGCCACCACGCCTTCAGCGACTACCAGTGGCTTGACGAC Fad2-F (TA515) Q508
321 CGGCCACCACGCCTTCAGCGACTACCAGTGGCTTGACGAC Fad2-F (GA908) Q4275

                370        380        390        400
361 ACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCCTT Fad2-D wt
361 ACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCCTT Fad2-D (GA316) IMC 129
361 ACCGTCGGTCTCATCTTCCACTCCTTCCTCCTCGTCCCTT Fad2-F wt
361 ACCGTCGGTCTCATCTTCCACTCCTTCCTCCTCGTCCCTT Fad2-F (TA515) Q508
361 ACCGTCGGTCTCATCTTCCACTCCTTCCTCCTCGTCCCTT Fad2-F (GA908) Q4275

                410        420        430        440
401 ACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAA Fad2-D wt
401 ACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAA Fad2-D (GA316) IMC 129
401 ACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAA Fad2-F wt
401 ACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAA Fad2-F (TA515) Q508
401 ACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAA Fad2-F (GA908) Q4275

                450        460        470        480
441 CACTGGCTCCCTCGAGAGACGAAGTGTTTGTCCCCAAG Fad2-D wt
441 CACTGGCTCCCTCGAGAGACGAAGTGTTTGTCCCCAAG Fad2-D (GA316) IMC 129
441 CACTGGCTCCCTCGAGAGACGAAGTGTTTGTCCCCAAG Fad2-F wt
441 CACTGGCTCCCTCGAGAGACGAAGTGTTTGTCCCCAAG Fad2-F (TA515) Q508
441 CACTGGCTCCCTCGAGAGACGAAGTGTTTGTCCCCAAG Fad2-F (GA908) Q4275
```

Fig. 2C

```
                490        500        510        520
481 AAGAAGTCAGACATCAAGTGGTACGGCAAGTACCTCAACA Fad2-D wt
481 AAGAAGTCAGACATCAAGTGGTACGGCAAGTACCTCAACA Fad2-D (GA316) IMC 129
481 AAGAAGTCAGACATCAAGTGGTACGGCAAGTACCTCAACA Fad2-F wt
481 AAGAAGTCAGACATCAAGTGGTACGGCAAGTACCACAACA Fad2-F (TA515) Q508
481 AAGAAGTCAGACATCAAGTGGTACGGCAAGTACCTCAACA Fad2-F (GA908) Q4275

                530        540        550        560
521 ACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCAC Fad2-D wt
521 ACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCAC Fad2-D (GA316) IMC 129
521 ACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCAC Fad2-F wt
521 ACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCAC Fad2-F (TA515) Q508
521 ACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCAC Fad2-F (GA908) Q4275

                570        580        590        600
561 TCTCGGCTGGCCTTTGTACTTAGCCTTCAACGTCTCGGGG Fad2-D wt
561 TCTCGGCTGGCCTTTGTACTTAGCCTTCAACGTCTCGGGG Fad2-D (GA316) IMC 129
561 TCTCGGCTGGCCTTTGTACTTAGCCTTCAACGTCTCGGGA Fad2-F wt
561 TCTCGGCTGGCCGTTGTACTTAGCCTTCAACGTCTCGGGA Fad2-F (TA515) Q508
561 TCTCGGCTGGCCGTTGTACTTAGCCTTCAACGTCTCGGGA Fad2-F (GA908) Q4275

                610        620        630        640
601 AGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCA Fad2-D wt
601 AGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCA Fad2-D (GA316) IMC 129
601 AGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCA Fad2-F wt
601 AGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCA Fad2-F (TA515) Q508
601 AGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCA Fad2-F (GA908) Q4275
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Fig. 2D

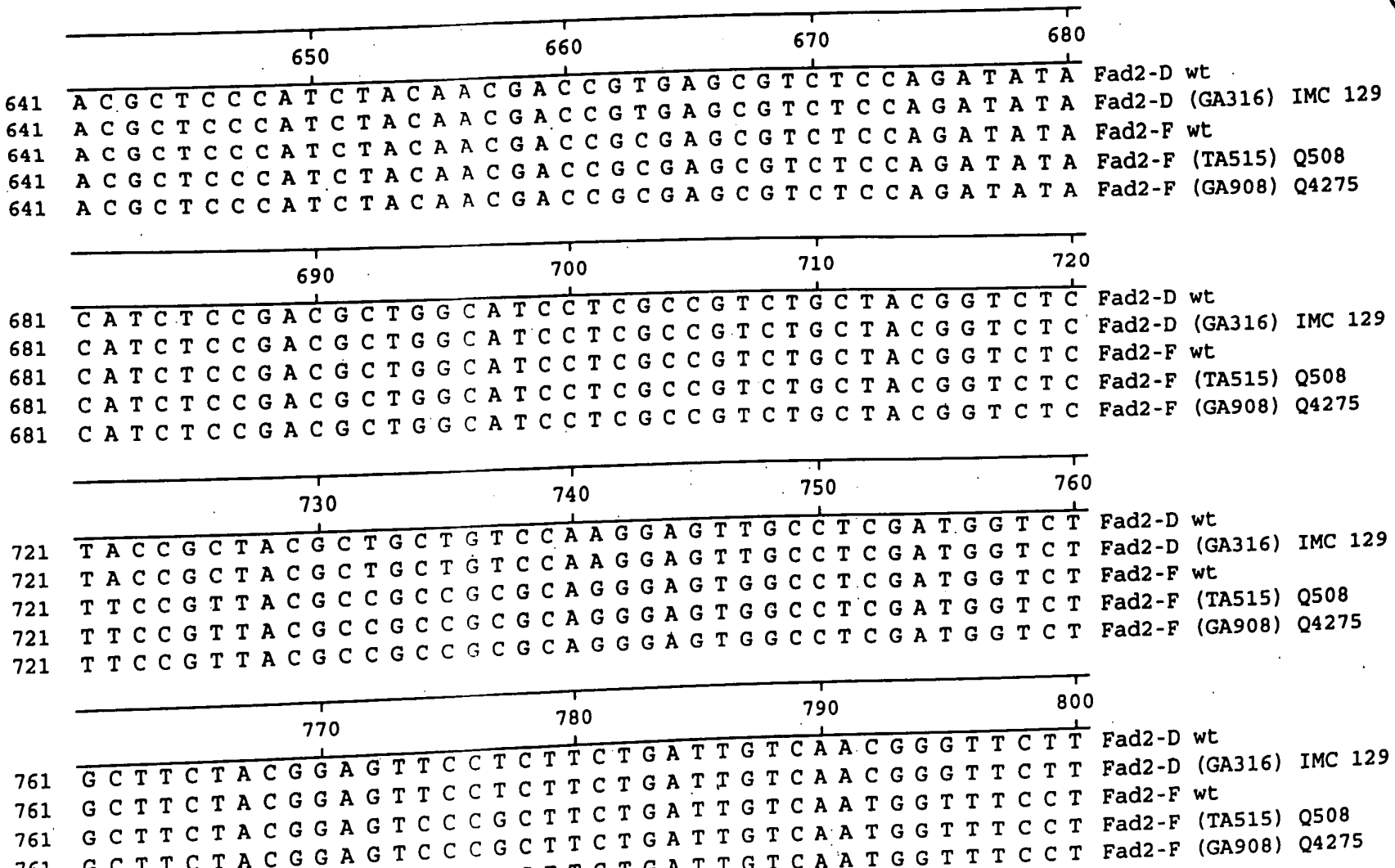

Fig. 2E

```
                810       820       830       840
801 AGTTTTGATCACTTACTTGCAGCACACGCATCCTTCCCTG Fad2-D wt
801 AGTTTTGATCACTTACTTGCAGCACACGCATCCTTCCCTG Fad2-D (GA316) IMC 129
801 CGTGTTGATCACTTACTTGCAGCACACGCATCCTTCCCTG Fad2-F wt
801 CGTGTTGATCACTTACTTGCAGCACACGCATCCTTCCCTG Fad2-F (TA515) Q508
801 CGTGTTGATCACTTACTTGCAGCACACGCATCCTTCCCTG Fad2-F (GA908) Q4275

                850       860       870       880
841 CCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAG Fad2-D wt
841 CCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAG Fad2-D (GA316) IMC 129
841 CCTCACTACGATTCGTCCGAGTGGGATTGGTTGAGGGGAG Fad2-F wt
841 CCTCACTACGATTCGTCCGAGTGGGATTGGTTGAGGGGAG Fad2-F (TA515) Q508
841 CCTCACTACGATTCGTCCGAGTGGGATTGGTTGAGGGGAG Fad2-F (GA908) Q4275

                890       900       910       920
881 CTTTGGCCACCGTTGACAGAGACTACGGAATCTTGAACAA Fad2-D wt
881 CTTTGGCCACCGTTGACAGAGACTACGGAATCTTGAACAA Fad2-D (GA316) IMC 129
881 CTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAA Fad2-F wt
881 CTTTGGCTACCGTTGACAGAGACTACGGAATCTTGAACAA Fad2-F (TA515) Q508
881 CTTTGGCTACCGTTGACAGAGACTACGAAATCTTGAACAA Fad2-F (GA908) Q4275

                930       940       950       960
921 GGTCTTCCACAATATCACGGACACGCACGTGGCGCATCAC Fad2-D wt
921 GGTCTTCCACAATATCACGGACACGCACGTGGCGCATCAC Fad2-D (GA316) IMC 129
921 GGTCTTCCACAATATTACCGACACGCACGTGGCGCATCAT Fad2-F wt
921 GGTCTTCCACAATATTACCGACACGCACGTGGCGCATCAT Fad2-F (TA515) Q508
921 GGTCTTCCACAATATTACCGACACGCACGTGGCGCATCAT Fad2-F (GA908) Q4275
```

Fig. 2F

	970 / 980 / 990 / 1000	
961	CTGTTCTCGACCATGCCGCATTATCATGCGATGGAAGCTA	Fad2-D wt
961	CTGTTCTCGACCATGCCGCATTATCATGCGATGGAAGCTA	Fad2-D (GA316) IMC 129
961	CTGTTCTCCACGATGCCGCATTATCACGCGATGGAAGCTA	Fad2-F wt
961	CTGTTCTCCACGATGCCGCATTATCACGCGATGGAAGCTA	Fad2-F (TA515) Q508
961	CTGTTCTCCACGATGCCGCATTATCACGCGATGGAAGCTA	Fad2-F (GA908) Q4275

	1010 / 1020 / 1030 / 1040	
1001	CGAAGGCGATAAAGCCGATACTGGGAGAGTATTATCAGTT	Fad2-D wt
1001	CGAAGGCGATAAAGCCGATACTGGGAGAGTATTATCAGTT	Fad2-D (GA316) IMC 129
1001	CCAAGGCGATAAAGCCGATACTGGGAGAGTATTATCAGTT	Fad2-F wt
1001	CCAAGGCGATAAAGCCGATACTGGGAGAGTATTATCAGTT	Fad2-F (TA515) Q508
1001	CCAAGGCGATAAAGCCGATACTGGGAGAGTATTATCAGTT	Fad2-F (GA908) Q4275

	1050 / 1060 / 1070 / 1080	
1041	CGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCG	Fad2-D wt
1041	CGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCG	Fad2-D (GA316) IMC 129
1041	CGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCG	Fad2-F wt
1041	CGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCG	Fad2-F (TA515) Q508
1041	CGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCG	Fad2-F (GA908) Q4275

Fig. 2G

```
                    1090      1100      1110      1120
1081 AAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGA Fad2-D wt
1081 AAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGA Fad2-D (GA316) IMC 129
1081 AAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGA Fad2-F wt
1081 AAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGA Fad2-F (TA515) Q508
1081 AAGGAGTGTATCTATGTGGAACCGGACAGGCAAGGTGAGA Fad2-F (GA908) Q4275

                    1130      1140      1150
1121 AGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA      Fad2-D wt
1121 AGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA      Fad2-D (GA316) IMC 129
1121 AGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA      Fad2-F wt
1121 AGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA      Fad2-F (TA515) Q508
1121 AGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA      Fad2-F (GA908) Q4275
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Fig. 2H

```
                    10                  20
                    |                   |
1   Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn  Fad2-D wt
1   Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn  Fad2-D (GA316) IMC129
1   Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr  Fad2-F wt
1   Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr  Fad2-F (TA515) Q508
1   Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr  Fad2-F (GA908) Q4275

                    30                  40
                    |                   |
21  Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  Fad2-D wt
21  Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  Fad2-D (GA316) IMC129
21  Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  Fad2-F wt
21  Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  Fad2-F (TA515) Q508
21  Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  Fad2-F (GA908) Q4275

                    50                  60
                    |                   |
41  Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile  Fad2-D wt
41  Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile  Fad2-D (GA316) IMC129
41  Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile  Fad2-F wt
41  Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile  Fad2-F (TA515) Q508
41  Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile  Fad2-F (GA908) Q4275

                    70                  80
                    |                   |
61  Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  Fad2-D wt
61  Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  Fad2-D (GA316) IMC129
61  Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  Fad2-F wt
61  Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  Fad2-F (TA515) Q508
61  Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  Fad2-F (GA908) Q4275
```

Fig. 3A

	90 ... 100	
81	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val	Fad2-D wt
81	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val	Fad2-D (GA316) IMC129
81	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val	Fad2-F wt
81	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val	Fad2-F (TA515) Q508
81	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val	Fad2-F (GA908) Q4275

	110 ... 120	
101	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	Fad2-D wt
101	Trp Val Ile Ala His Lys Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	Fad2-D (GA316) IMC129
101	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	Fad2-F wt
101	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	Fad2-F (TA515) Q508
101	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp	Fad2-F (GA908) Q4275

	130 ... 140	
121	Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	Fad2-D wt
121	Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	Fad2-D (GA316) IMC129
121	Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	Fad2-F wt
121	Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	Fad2-F (TA515) Q508
121	Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser	Fad2-F (GA908) Q4275

	150 ... 160	
141	His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	Fad2-D wt
141	His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	Fad2-D (GA316) IMC129
141	His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	Fad2-F wt
141	His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	Fad2-F (TA515) Q508
141	His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	Fad2-F (GA908) Q4275

Fig. 3B

		170	180	
161	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys	Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val	Fad2-D wt
161	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys	Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val	Fad2-D (GA316) IMC129
161	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys	Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val	Fad2-F wt
161	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys	Tyr His Asn Asn Pro Leu Gly Arg Thr Val	Fad2-F (TA515) Q508
161	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys	Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val	Fad2-F (GA908) Q4275

	190	200	
181	Met Leu Thr Val Gln Phe Thr Leu Gly Trp	Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	Fad2-D wt
181	Met Leu Thr Val Gln Phe Thr Leu Gly Trp	Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	Fad2-D (GA316) IMC129
181	Met Leu Thr Val Gln Phe Thr Leu Gly Trp	Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	Fad2-F wt
181	Met Leu Thr Val Gln Phe Thr Leu Gly Trp	Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	Fad2-F (TA515) Q508
181	Met Leu Thr Val Gln Phe Thr Leu Gly Trp	Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly	Fad2-F (GA908) Q4275

	210	220	
201	Arg Pro Tyr Asp Gly Gly Phe Ala Cys His	Phe His Pro Asn Ala Pro Ile Tyr Asn Asp	Fad2-D wt
201	Arg Pro Tyr Asp Gly Gly Phe Ala Cys His	Phe His Pro Asn Ala Pro Ile Tyr Asn Asp	Fad2-D (GA316) IMC129
201	Arg Pro Tyr Asp Gly Gly Phe Ala Cys His	Phe His Pro Asn Ala Pro Ile Tyr Asn Asp	Fad2-F wt
201	Arg Pro Tyr Asp Gly Gly Phe Ala Cys His	Phe His Pro Asn Ala Pro Ile Tyr Asn Asp	Fad2-F (TA515) Q508
201	Arg Pro Tyr Asp Gly Gly Phe Ala Cys His	Phe His Pro Asn Ala Pro Ile Tyr Asn Asp	Fad2-F (GA908) Q4275

	230	240	
221	Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp	Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	Fad2-D wt
221	Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp	Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	Fad2-D (GA316) IMC129
221	Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp	Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	Fad2-F wt
221	Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp	Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	Fad2-F (TA515) Q508
221	Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp	Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	Fad2-F (GA908) Q4275

Fig. 3C

	250 … 260	
241	Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu	Fad2-D wt
241	Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu	Fad2-D (GA316) IMC129
241	Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu	Fad2-F wt
241	Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu	Fad2-F (TA515) Q508
241	Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu	Fad2-F (GA908) Q4275

	270 … 280	
261	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu	Fad2-D wt
261	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu	Fad2-D (GA316) IMC129
261	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu	Fad2-F wt
261	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu	Fad2-F (TA515) Q508
261	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu	Fad2-F (GA908) Q4275

	290 … 300	
281	Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg	Fad2-D wt
281	Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg	Fad2-D (GA316) IMC129
281	Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg	Fad2-F wt
281	Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg	Fad2-F (TA515) Q508
281	Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg	Fad2-F (GA908) Q4275

	310 … 320	
301	Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	Fad2-D wt
301	Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	Fad2-D (GA316) IMC129
301	Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	Fad2-F wt
301	Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	Fad2-F (TA515) Q508
301	Asp Tyr Glu Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	Fad2-F (GA908) Q4275

Fig. 3D

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                                        330                                     340
321 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  Fad2-D wt
321 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  Fad2-D (GA316) IMC129
321 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  Fad2-F wt
321 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  Fad2-F (TA515) Q508
321 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile  Fad2-F (GA908) Q4275

                                        350                                     360
341 Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala  Fad2-D wt
341 Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala  Fad2-D (GA316) IMC129
341 Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala  Fad2-F wt
341 Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala  Fad2-F (TA515) Q508
341 Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala  Fad2-F (GA908) Q4275

                                        370                                     380
361 Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr  Fad2-D wt
361 Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr  Fad2-D (GA316) IMC129
361 Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr  Fad2-F wt
361 Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr  Fad2-F (TA515) Q508
361 Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr  Fad2-F (GA908) Q4275

381 Asn Asn Lys Leu ter                                                              Fad2-D wt
381 Asn Asn Lys Leu ter                                                              Fad2-D (GA316) IMC129
381 Asn Asn Lys Leu ter                                                              Fad2-F wt
381 Asn Asn Lys Leu ter                                                              Fad2-F (TA515) Q508
381 Asn Asn Lys Leu ter                                                              Fad2-F (GA908) Q4275
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Fig. 3E